



SEQUENCE LISTING

<110> Yamamoto, Satoshi
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<120> METHOD FOR IDENTIFICATION AND DETECTION OF MICROORGANISMS
USING GYRASE GENE AS AN INDICATOR

<130> 12817-004001

<140> US 09/823,829

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<150> US 09/208,688

<151> 1998-12-10

<150> JP 97/343316

<151> 1997-12-12

<160> 82

<170> PatentIn version 2.0

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<212> DNA

<213> Bacteroides vulgatus

<220>

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Ser	Cys	Val	Asn	Ala	Leu	Ser	Thr	His	Met	Thr	Thr	Gln	Val	Phe	Arg	
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ggt	ggc	aag	atc	tac	cag	cag	gaa	tac	agc	tgc	gga	cat	cct	ttg	tat	144
Gly	Gly	Lys	Ile	Tyr	Gln	Gln	Glu	Tyr	Ser	Cys	Gly	His	Pro	Leu	Tyr	
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Phe	Trp	Pro	Asp	Asp	Thr	Ile	Phe	Thr	Val	Thr	Glu	Tyr	Lys	Phe	Asp	
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Ile Leu Gln Ala Arg Met Arg Glu Leu Ala Tyr Leu Asn Lys Gly Ile	
85 90 95	
acc att tca ctg acc gac cgc cgg atc aaa gaa gaa gat ggc agc ttc	336
Thr Ile Ser Leu Thr Asp Arg Arg Ile Lys Glu Glu Asp Gly Ser Phe	
100 105 110	
aag aaa gaa ata ttc cat tcg gac gaa gga gtg aaa gag ttt gta cgt	384
Lys Lys Glu Ile Phe His Ser Asp Glu Gly Val Lys Glu Phe Val Arg	
115 120 125	
ttc ctg aac cgt aac aac gaa gcg ctg att aat gat gtc att tat ctg	432
Phe Leu Asn Arg Asn Asn Glu Ala Leu Ile Asn Asp Val Ile Tyr Leu	
130 135 140	
aat acc gaa aaa aac aat acc ccc att gaa tgt gcc atc atg tac aat	480
Asn Thr Glu Lys Asn Asn Thr Pro Ile Glu Cys Ala Ile Met Tyr Asn	
145 150 155 160	
aca ggc tat cgt gaa agc ctg cat tcg tat gta aac aat atc aat aca	528
Thr Gly Tyr Arg Glu Ser Leu His Ser Tyr Val Asn Asn Ile Asn Thr	
165 170 175	
ata gaa ggc ggt aca cac gag gcc ggt ttc cgc agc gca tta acc cgt	576
Ile Glu Gly Gly Thr His Glu Ala Gly Phe Arg Ser Ala Leu Thr Arg	
180 185 190	
gta ctg aag aaa tat gcg gaa gat acc aaa gca ctg gaa aaa gca aaa	624
Val Leu Lys Lys Tyr Ala Glu Asp Thr Lys Ala Leu Glu Lys Ala Lys	
195 200 205	
gtc gag att tcg gga gag gac ttc cgc gaa ggc ttg att gcc gtc att	672
Val Glu Ile Ser Gly Glu Asp Phe Arg Glu Gly Leu Ile Ala Val Ile	
210 215 220	
tca gtg aaa gta gcc gag ccg cag ttc gaa gga cag acc aag acc aag	720
Ser Val Lys Val Ala Glu Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys	
225 230 235 240	
ctg ggc aac agc gaa gtg agt ggt gcc gtg aac caa gct gta ggc gaa	768
Leu Gly Asn Ser Glu Val Ser Gly Ala Val Asn Gln Ala Val Gly Glu	
245 250 255	
gcg ctt aca tat tat ctg gaa gaa cat ccg aaa gaa gca aaa cag att	816
Ala Leu Thr Tyr Tyr Leu Glu Glu His Pro Lys Glu Ala Lys Gln Ile	
260 265 270	
gtt gac aaa gtg atc ctg gct gca aca gcg cgt atc gcc gca cgc aag	864
Val Asp Lys Val Ile Leu Ala Ala Thr Ala Arg Ile Ala Ala Arg Lys	
275 280 285	
gca cgt gaa tct gtt caa aga aag agt ccg atg ggc ggt ggc gga ctg	912
Ala Arg Glu Ser Val Gln Arg Lys Ser Pro Met Gly Gly Gly Gly Leu	
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ccg ggc aaa ctg gcc gac tgc tcg agc cgt aat ccg gag gaa tgt gaa	960

Pro Gly Lys Leu Ala Asp Cys Ser Ser Arg Asn Pro Glu Glu Cys Glu
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cta ttc ctg gtc gag ggt gac tcg gca ggt ggt tct gcc aag caa gga 1008
 Leu Phe Leu Val Glu Gly Asp Ser Ala Gly Gly Ser Ala Lys Gln Gly
 325 330 335

cgt agc cgt gcc ttc cag gca att cta cct ttg agg ggt aaa atc ctg 1056
 Arg Ser Arg Ala Phe Gln Ala Ile Leu Pro Leu Arg Gly Lys Ile Leu
 340 345 350

aat gtg gaa aaa gcg atg tgg cac aag gct ttt gaa agc gat gag gtc 1104
 Asn Val Glu Lys Ala Met Trp His Lys Ala Phe Glu Ser Asp Glu Val
 355 360 365

aat aat atc atc acc gcc ctg ggt gtc cgt ttc ggt gtg gac gga aat 1152
 Asn Asn Ile Ile Thr Ala Leu Gly Val Arg Phe Gly Val Asp Gly Asn
 370 375 380

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<213> Bacteroides vulgatus

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 Gly Gly Lys Ile Tyr Gln Gln Glu Tyr Ser Cys Gly His Pro Leu Tyr
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 Ser Val Lys Glu Val Gly Thr Ala Asp Ile Thr Gly Thr Lys Gln Thr
 50 55 60
 Phe Trp Pro Asp Asp Thr Ile Phe Thr Val Thr Glu Tyr Lys Phe Asp
 65 70 75 80
 Ile Leu Gln Ala Arg Met Arg Glu Leu Ala Tyr Leu Asn Lys Gly Ile
 85 90 95
 Thr Ile Ser Leu Thr Asp Arg Arg Ile Lys Glu Glu Asp Gly Ser Phe
 100 105 110
 Lys Lys Glu Ile Phe His Ser Asp Glu Gly Val Lys Glu Phe Val Arg
 115 120 125
 Phe Leu Asn Arg Asn Asn Glu Ala Leu Ile Asn Asp Val Ile Tyr Leu
 130 135 140
 Asn Thr Glu Lys Asn Asn Thr Pro Ile Glu Cys Ala Ile Met Tyr Asn
 145 150 155 160
 Thr Gly Tyr Arg Glu Ser Leu His Ser Tyr Val Asn Asn Ile Asn Thr
 165 170 175
 Ile Glu Gly Gly Thr His Glu Ala Gly Phe Arg Ser Ala Leu Thr Arg
 180 185 190

Val Leu Lys Lys Tyr Ala Glu Asp Thr Lys Ala Leu Glu Lys Ala Lys
 195 200 205
 Val Glu Ile Ser Gly Glu Asp Phe Arg Glu Gly Leu Ile Ala Val Ile
 210 215 220
 Ser Val Lys Val Ala Glu Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys
 225 230 235 240
 Leu Gly Asn Ser Glu Val Ser Gly Ala Val Asn Gln Ala Val Gly Glu
 245 250 255
 Ala Leu Thr Tyr Tyr Leu Glu Glu His Pro Lys Glu Ala Lys Gln Ile
 260 265 270
 Val Asp Lys Val Ile Leu Ala Ala Thr Ala Arg Ile Ala Ala Arg Lys
 275 280 285
 Ala Arg Glu Ser Val Gln Arg Lys Ser Pro Met Gly Gly Gly Gly Leu
 290 295 300
 Pro Gly Lys Leu Ala Asp Cys Ser Ser Arg Asn Pro Glu Glu Cys Glu
 305 310 315 320
 Leu Phe Leu Val Glu Gly Asp Ser Ala Gly Gly Ser Ala Lys Gln Gly
 325 330 335
 Arg Ser Arg Ala Phe Gln Ala Ile Leu Pro Leu Arg Gly Lys Ile Leu
 340 345 350
 Asn Val Glu Lys Ala Met Trp His Lys Ala Phe Glu Ser Asp Glu Val
 355 360 365
 Asn Asn Ile Ile Thr Ala Leu Gly Val Arg Phe Gly Val Asp Gly Asn
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 Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Asn Val Lys
 20 25 30
 cgt gac ggc tat gag tgg ttc cag tac tac gac cgg gcg gtg ccc ggc 144
 Arg Asp Gly Tyr Glu Trp Phe Gln Tyr Tyr Asp Arg Ala Val Pro Gly
 35 40 45
 acc ctc aag caa ggc gag gcg acc aag aag acc ggc acc acg atc cgg 192
 Thr Leu Lys Gln Gly Glu Ala Thr Lys Lys Thr Gly Thr Thr Ile Arg
 50 55 60
 ttc tgg gcc gat cct gag atc ttc gaa acc acc cag tac gac ttc gag 240
 Phe Trp Ala Asp Pro Glu Ile Phe Glu Thr Thr Gln Tyr Asp Phe Glu

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acg gtg gcg cgc cgg ttg cag gaa atg gcg ttc ctc aac aag ggc ctg				288
Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu	85	90	95	
acc atc aac ctc acc gac gaa cgt gtc gag cag gac gag gtg gtc gat				336
Thr Ile Asn Leu Thr Asp Glu Arg Val Glu Gln Asp Glu Val Val Asp	100	105	110	
gag gtg gtt agc gac acc gcc gag gcg ccg aag tca gcc gag gag cag				384
Glu Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Glu Glu Gln	115	120	125	
gcg gcc gaa tcg gcc aag ccg cac aag gtc aag cac cgc acg ttc cac				432
Ala Ala Glu Ser Ala Lys Pro His Lys Val Lys His Arg Thr Phe His	130	135	140	
tac ccg ggt ggg ttg gtg gat ttc gtc aag cac atc aat cgc acc aaa				480
Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys	145	150	155	160
aac ccg atc cag cag agc gtc atc gac ttc gac ggc aaa gga acc ggg				528
Asn Pro Ile Gln Gln Ser Val Ile Asp Phe Asp Gly Lys Gly Thr Gly	165	170	175	
cac gaa gtc gag atc gcg atg cag tgg aac ggt ggt tat tcg gag tcg				576
His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser	180	185	190	
gtg cac acc ttc gcc aac acc atc aac acc cat gag ggc ggc acc cac				624
Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His	195	200	205	
gag gag ggc ttc cgc agc gcg ctg acc tcg gtg gtg aac aag tac gcc				672
Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala	210	215	220	
aaa gac aag aag ctg ctc aag gac aag gat ccc aac ctc acc ggc gac				720
Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp	225	230	235	240
gac atc cga gaa ggg ctg gcc gcg gtg atc tcc gtg aag gtc gcc gag				768
Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ala Glu	245	250	255	
ccg cag ttc gag ggc cag act aag acg aaa ctc ggc aac acc gag gtc				816
Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val	260	265	270	
aag tcg ttt gtc cag aaa gtc tgt aac gaa caa ctc act cac tgg ttc				864
Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe	275	280	285	
gag gcg aac ccg tcg gaa gct aaa acc gtt gta aac aag gcg gtt tcg				912
Glu Ala Asn Pro Ser Glu Ala Lys Thr Val Val Asn Lys Ala Val Ser	290	295	300	

tcg gcc cag gcc cgc att gcg gcg cgt aag gcg cgg gag ttg gtg cgg 960
 Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg
 305 310 315 320

cgt aag agt gct acg gat ttg ggt ggg ttg ccg ggc aag ttg gct gat 1008
 Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp
 325 330 335

tgc cgc tcg acg gat ccg cgg aag tct gag ctg tat gtg gtg gaa ggt 1056
 Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly
 340 345 350

gat tcc gcg ggt ggg tcg gcg aaa agt ggg cgt gat tcg atg ttc cag 1104
 Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln
 355 360 365

gcg atc ttg ccg ctg cgc ggc aag atc atc aac gtc gaa aag gcc cgc 1152
 Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg
 370 375 380

atc gat cgg gtg ctg aaa aac acc gaa gtc cag gcc atc atc acc gcg 1200
 Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala
 385 390 395 400

ctg ggc acc ggc atc cac gac gaa ttc gac atc acc aaa ctg cgt tac 1248
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cac aag atc gtg ttg 1263
 His Lys Ile Val Leu
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<210> 4

<211> 421

<212> PRT

<213> Mycobacterium simiae

<400> 4

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 35 40 45
 Thr Leu Lys Gln Gly Glu Ala Thr Lys Lys Thr Gly Thr Thr Ile Arg
 50 55 60
 Phe Trp Ala Asp Pro Glu Ile Phe Glu Thr Thr Gln Tyr Asp Phe Glu
 65 70 75 80
 Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu
 85 90 95
 Thr Ile Asn Leu Thr Asp Glu Arg Val Glu Gln Asp Glu Val Val Asp
 100 105 110
 Glu Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Glu Glu Gln
 115 120 125
 Ala Ala Glu Ser Ala Lys Pro His Lys Val Lys His Arg Thr Phe His
 130 135 140

Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys
 145 150 155 160
 Asn Pro Ile Gln Gln Ser Val Ile Asp Phe Asp Gly Lys Gly Thr Gly
 165 170 175
 His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser
 180 185 190
 Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His
 195 200 205
 Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala
 210 215 220
 Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp
 225 230 235 240
 Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ala Glu
 245 250 255
 Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Thr Glu Val
 260 265 270
 Lys Ser Phe Val Gln Lys Val Cys Asn Glu Gln Leu Thr His Trp Phe
 275 280 285
 Glu Ala Asn Pro Ser Glu Ala Lys Thr Val Val Asn Lys Ala Val Ser
 290 295 300
 Ser Ala Gln Ala Arg Ile Ala Ala Arg Lys Ala Arg Glu Leu Val Arg
 305 310 315 320
 Arg Lys Ser Ala Thr Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp
 325 330 335
 Cys Arg Ser Thr Asp Pro Arg Lys Ser Glu Leu Tyr Val Val Glu Gly
 340 345 350
 Asp Ser Ala Gly Gly Ser Ala Lys Ser Gly Arg Asp Ser Met Phe Gln
 355 360 365
 Ala Ile Leu Pro Leu Arg Gly Lys Ile Ile Asn Val Glu Lys Ala Arg
 370 375 380
 Ile Asp Arg Val Leu Lys Asn Thr Glu Val Gln Ala Ile Ile Thr Ala
 385 390 395 400
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 405 410 415
 His Lys Ile Val Leu
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 <213> Chitinophaga pinensis

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 gat aag aac aaa atg ttc gaa aaa acc aag atc gaa gta aca ggt gat 96
 Asp Lys Asn Lys Met Phe Glu Lys Thr Lys Ile Glu Val Thr Gly Asp
 20 25 30
 gac ttc cgt gaa ggt ctg agc gct atc atc agc gta aaa gta cct gaa 144
 Asp Phe Arg Glu Gly Leu Ser Ala Ile Ile Ser Val Lys Val Pro Glu

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Pro Gln Phe Glu Gly Gln Thr Lys Thr Lys Leu Gly Asn Ser Asp Val			
50	55	60	
atg ggg gtt gtg gac agt tcc gta gca gcc gta ctg gat gcc tac ctg			240
Met Gly Val Val Asp Ser Ser Val Ala Ala Val Leu Asp Ala Tyr Leu			
65	70	75	80
gaa gaa cat ccc cgc gaa gcc aag atc att atc aat aaa gtg gta ctg			288
Glu Glu His Pro Arg Glu Ala Lys Ile Ile Ile Asn Lys Val Val Leu			
	85	90	95
gca gca cag gcg cgt gaa gca gcc cgt aaa gca cgc cag atg gta cag			336
Ala Ala Gln Ala Arg Glu Ala Ala Arg Lys Ala Arg Gln Met Val Gln			
	100	105	110
cgt aag agc gta ctg agt gga agc ggc ttg oct ggt aaa ctg gct gac			384
Arg Lys Ser Val Leu Ser Gly Ser Gly Leu Pro Gly Lys Leu Ala Asp			
	115	120	125
tgc tct gaa aat gat cct gaa aaa tgt gaa ctg tac ctg gta gag ggt			432
Cys Ser Glu Asn Asp Pro Glu Lys Cys Glu Leu Tyr Leu Val Glu Gly			
	130	135	140
gac tcc gca ggt ggt acg gct aaa caa gga cgt aac cgt agc ttc cag			480
Asp Ser Ala Gly Gly Thr Ala Lys Gln Gly Arg Asn Arg Ser Phe Gln			
	145	150	155
gcg atc ctg ccg ctc agg ggt aaa atc ctg aac gtg gag aaa gcc atg			528
Ala Ile Leu Pro Leu Arg Gly Lys Ile Leu Asn Val Glu Lys Ala Met			
	165	170	175
gag cat aag ata tat gag aat gag gag att aaa aac atc ttc acc gca			576
Glu His Lys Ile Tyr Glu Asn Glu Glu Ile Lys Asn Ile Phe Thr Ala			
	180	185	190
ctt ggt gta acc atc ggt acg gaa gaa gat gac aaa gcc ctc aac ctc			624
Leu Gly Val Thr Ile Gly Thr Glu Glu Asp Asp Lys Ala Leu Asn Leu			
	195	200	205
tcc aaa ctg cgc tat cac aaa ctg atc atc atg acg			660
Ser Lys Leu Arg Tyr His Lys Leu Ile Ile Met Thr			
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Asp Phe Arg Glu Gly Leu Ser Ala Ile Ile Ser Val Lys Val Pro Glu			

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 Ile Thr Ile Thr Leu Thr Asp Lys Arg His Thr Lys Asp Asn Gly Asp
 100 105 110

ttt gaa ggt gaa gtt ttt cat tct aaa gaa ggg ctt aaa gaa ttc gtt 384
 Phe Glu Gly Glu Val Phe His Ser Lys Glu Gly Leu Lys Glu Phe Val
 115 120 125

cga ttt tta gat gct ggt aga gaa cca att att tct cac gta ata agc 432
 Arg Phe Leu Asp Ala Gly Arg Glu Pro Ile Ile Ser His Val Ile Ser
 130 135 140

atg gag cac gaa aaa gga gaa gtt cct gtt gag gtt gct ctt gtt tac 480
 Met Glu His Glu Lys Gly Glu Val Pro Val Glu Val Ala Leu Val Tyr
 145 150 155 160

aat aca agt tac tcc gaa aat att ttc tct tac gta aat aat att aac 528
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<211> 179

<212> PRT

<213> Flavobacterium aquatile

<400> 8

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Asp Gly Lys Val Tyr Glu Gln Glu Tyr Glu Lys Gly Lys Ala Met Tyr
 35 40 45

Pro Val Lys Gln Val Gly Glu Thr Thr Lys Arg Gly Thr Met Val Thr
 50 55 60

Phe His Pro Asp Lys Thr Ile Phe Thr Gln Thr Ile Glu Tyr Ser Tyr
 65 70 75 80

Asp Thr Leu Ala Ala Arg Met Arg Glu Leu Ser Phe Leu Asn Lys Gly
 85 90 95

Ile Thr Ile Thr Leu Thr Asp Lys Arg His Thr Lys Asp Asn Gly Asp
 100 105 110

Phe Glu Gly Glu Val Phe His Ser Lys Glu Gly Leu Lys Glu Phe Val
 115 120 125

Arg Phe Leu Asp Ala Gly Arg Glu Pro Ile Ile Ser His Val Ile Ser
 130 135 140

Met Glu His Glu Lys Gly Glu Val Pro Val Glu Val Ala Leu Val Tyr
 145 150 155 160

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Thr His Glu

<210> 9

<211> 783
 <212> DNA
 <213> Mycobacterium asiaticum

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 <222> (1)...(783)

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gtg tcg gtg gtc aac gcg ctg tcc acc cgc ctg gag gtc acc atc aag	96
Val Ser Val Val Asn Ala Leu Ser Thr Arg Leu Glu Val Thr Ile Lys	
20 25 30	
cgc gac ggg cac gag tgg ttt cag tac tac gac cgc gcc gtg ccc gga	144
Arg Asp Gly His Glu Trp Phe Gln Tyr Tyr Asp Arg Ala Val Pro Gly	
35 40 45	
acc ctc aag cag ggc gag gcc acc aag aag acc gga acc acg atc agg	192
Thr Leu Lys Gln Gly Glu Ala Thr Lys Lys Thr Gly Thr Thr Ile Arg	
50 55 60	
ttc tgg gcg gac ccc gaa atc ttc gaa acc aca cag tac gac ttc gag	240
Phe Trp Ala Asp Pro Glu Ile Phe Glu Thr Thr Gln Tyr Asp Phe Glu	
65 70 75 80	
acc gtg gcg cgg cgg ctg cag gag atg gcc ttc ctc aac aag ggc ctc	288
Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu	
85 90 95	
acc atc aac ctc acc gac gaa cga gtg gag cag gac gag gtc gtc gac	336
Thr Ile Asn Leu Thr Asp Glu Arg Val Glu Gln Asp Glu Val Val Asp	
100 105 110	
gag gtc gtc agc gac acc gcc gag gca ccg aag tcc gcc gaa gag aag	384
Glu Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Glu Glu Lys	
115 120 125	
gcc gcg gaa tcg act gcg cca cac aag gtc aag cac cgc acc ttc cac	432
Ala Ala Glu Ser Thr Ala Pro His Lys Val Lys His Arg Thr Phe His	
130 135 140	
tac ccc ggc ggt ctg gtc gac ttc gtc aag cac atc aac cgc acc aag	480
Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys	
145 150 155 160	
agc ccg atc cag cag agc gtc atc gat ttc gac ggc aag ggc acc ggc	528
Ser Pro Ile Gln Gln Ser Val Ile Asp Phe Asp Gly Lys Gly Thr Gly	
165 170 175	
cac gag gtc gag atc gcc atg cag tgg aac ggc ggc tac tcg gag tcc	576
His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser	
180 185 190	

gtc cac acc ttc gcc aac acc atc aac acg cac gag ggc ggc acc cac	624
Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His	
195 200 205	
gag gag ggc ttc cgc agc gcg ctg acg tcg gtg gtg aac aag tac gcc	672
Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala	
210 215 220	
aaa gac aag aaa ctg ctg aag gac aaa gat ccc aac ctc acc ggt gac	720
Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp	
225 230 235 240	
gac atc cgt gag ggc ttg gcc gcg gtc atc tcg gtg aag gtc gcc gag	768
Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ala Glu	
245 250 255	
cca cag ttc gaa ggc	783
Pro Gln Phe Glu Gly	
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<210> 10

<211> 261

<212> PRT

<213> Mycobacterium asiaticum

<400> 10

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35 40 45	
Thr Leu Lys Gln Gly Glu Ala Thr Lys Lys Thr Gly Thr Thr Ile Arg	
50 55 60	
Phe Trp Ala Asp Pro Glu Ile Phe Glu Thr Thr Gln Tyr Asp Phe Glu	
65 70 75 80	
Thr Val Ala Arg Arg Leu Gln Glu Met Ala Phe Leu Asn Lys Gly Leu	
85 90 95	
Thr Ile Asn Leu Thr Asp Glu Arg Val Glu Gln Asp Glu Val Val Asp	
100 105 110	
Glu Val Val Ser Asp Thr Ala Glu Ala Pro Lys Ser Ala Glu Glu Lys	
115 120 125	
Ala Ala Glu Ser Thr Ala Pro His Lys Val Lys His Arg Thr Phe His	
130 135 140	
Tyr Pro Gly Gly Leu Val Asp Phe Val Lys His Ile Asn Arg Thr Lys	
145 150 155 160	
Ser Pro Ile Gln Gln Ser Val Ile Asp Phe Asp Gly Lys Gly Thr Gly	
165 170 175	
His Glu Val Glu Ile Ala Met Gln Trp Asn Gly Gly Tyr Ser Glu Ser	
180 185 190	
Val His Thr Phe Ala Asn Thr Ile Asn Thr His Glu Gly Gly Thr His	
195 200 205	
Glu Glu Gly Phe Arg Ser Ala Leu Thr Ser Val Val Asn Lys Tyr Ala	
210 215 220	
Lys Asp Lys Lys Leu Leu Lys Asp Lys Asp Pro Asn Leu Thr Gly Asp	
225 230 235 240	
Asp Ile Arg Glu Gly Leu Ala Ala Val Ile Ser Val Lys Val Ala Glu	

Pro Gln Phe Glu Gly 245 250 255
260

<210> 11
<211> 195
<212> DNA
<213> Cytophaga lytica

<220>
<221> CDS
<222> (1)...(195)

<400> 11
agc cac att gaa act tta att ctt aca ttc ttc ttc cgt ttt atg cga 48
Ser His Ile Glu Thr Leu Ile Leu Thr Phe Phe Phe Arg Phe Met Arg
1 5 10 15
gaa cta ata gaa ggc gga cac gtt tac ata gca aca cca cct tta tat 96
Glu Leu Ile Glu Gly Gly His Val Tyr Ile Ala Thr Pro Pro Leu Tyr
20 25 30
tta gtt aaa aaa gga act aaa aag cgt tat gct tgg aat gat aaa gaa 144
Leu Val Lys Lys Gly Thr Lys Lys Arg Tyr Ala Trp Asn Asp Lys Glu
35 40 45
cga gat gaa ata gca gat agc ttt aat ggt agt gta ggt atc caa aga 192
Arg Asp Glu Ile Ala Asp Ser Phe Asn Gly Ser Val Gly Ile Gln Arg
50 55 60
tat 195
Tyr
65

<210> 12
<211> 65
<212> PRT
<213> Cytophaga lytica

<400> 12
Ser His Ile Glu Thr Leu Ile Leu Thr Phe Phe Phe Arg Phe Met Arg
1 5 10 15
Glu Leu Ile Glu Gly Gly His Val Tyr Ile Ala Thr Pro Pro Leu Tyr
20 25 30
Leu Val Lys Lys Gly Thr Lys Lys Arg Tyr Ala Trp Asn Asp Lys Glu
35 40 45
Arg Asp Glu Ile Ala Asp Ser Phe Asn Gly Ser Val Gly Ile Gln Arg
50 55 60
Tyr
65

<210> 13
<211> 1170
<212> DNA
<213> Synechococcus sp.

<220>

<221> CDS

<222> (1)...(1170)

<400> 13

gtg	gtg	gac	aac	gcc	gtc	gac	aaa	gcc	ttg	gcg	ggc	tac	tgc	aat	acc	48
Val	Val	Asp	Asn	Ala	Val	Asp	Lys	Ala	Leu	Ala	Gly	Tyr	Cys	Asn	Thr	
1				5					10					15		
att	gat	gtt	cgt	ctg	ctc	aaa	gac	ggc	tcc	tgc	caa	gtc	acc	gat	aac	96
Ile	Asp	Val	Arg	Leu	Leu	Lys	Asp	Gly	Ser	Cys	Gln	Val	Thr	Asp	Asn	
			20					25					30			
ggt	cgc	ggc	att	ccc	aca	gat	att	cac	ccc	caa	acc	ggg	aag	tct	gct	144
Gly	Arg	Gly	Ile	Pro	Thr	Asp	Ile	His	Pro	Gln	Thr	Gly	Lys	Ser	Ala	
		35					40					45				
ctc	gaa	acc	gtg	ctg	acg	att	ctg	cac	gcg	ggc	ggc	aag	ttt	ggc	ggt	192
Leu	Glu	Thr	Val	Leu	Thr	Ile	Leu	His	Ala	Gly	Gly	Lys	Phe	Gly	Gly	
	50					55					60					
ggc	ggt	tat	aag	gtg	tcg	ggg	ggt	ctg	cac	ggc	gtc	ggt	gtg	tct	gtc	240
Gly	Gly	Tyr	Lys	Val	Ser	Gly	Gly	Leu	His	Gly	Val	Gly	Val	Ser	Val	
	65				70					75					80	
gtc	aac	gcc	ctc	tca	gaa	tat	gtc	gaa	gtc	acc	gtg	tgg	cgg	gaa	ggc	288
Val	Asn	Ala	Leu	Ser	Glu	Tyr	Val	Glu	Val	Thr	Val	Trp	Arg	Glu	Gly	
				85					90					95		
aaa	acc	cac	caa	cag	cgc	ttt	gaa	cag	ggc	aac	ccg	atc	ggg	gag	ttg	336
Lys	Thr	His	Gln	Gln	Arg	Phe	Glu	Gln	Gly	Asn	Pro	Ile	Gly	Glu	Leu	
			100					105					110			
caa	gtt	gcc	ccg	gat	gcc	gac	gat	cgc	cgc	ggg	aca	caa	gtt	cgt	ttc	384
Gln	Val	Ala	Pro	Asp	Ala	Asp	Asp	Arg	Arg	Gly	Thr	Gln	Val	Arg	Phe	
		115					120					125				
aaa	cca	gac	gcc	acg	atc	ttt	tct	gaa	aca	acc	gag	ttc	gat	tac	ggc	432
Lys	Pro	Asp	Ala	Thr	Ile	Phe	Ser	Glu	Thr	Thr	Glu	Phe	Asp	Tyr	Gly	
	130					135					140					
acc	cta	gca	agc	cga	ttg	aag	gag	cta	gcc	tat	ctg	aat	gcg	ggc	gtc	480
Thr	Leu	Ala	Ser	Arg	Leu	Lys	Glu	Leu	Ala	Tyr	Leu	Asn	Ala	Gly	Val	
	145				150				155						160	
cgc	atc	gac	ttt	acc	gat	gag	cgg	ctg	cag	ctc	acc	aag	aat	cac	gag	528
Arg	Ile	Asp	Phe	Thr	Asp	Glu	Arg	Leu	Gln	Leu	Thr	Lys	Asn	His	Glu	
				165					170					175		
ccc	cat	caa	gaa	acc	tat	tac	ttt	gaa	ggc	ggt	att	cgc	gaa	tac	gtc	576
Pro	His	Gln	Glu	Thr	Tyr	Tyr	Phe	Glu	Gly	Gly	Ile	Arg	Glu	Tyr	Val	
			180					185					190			
gcc	tac	atg	aat	acc	gat	aaa	cag	gcg	ctg	cac	tca	gag	att	atc	ttt	624
Ala	Tyr	Met	Asn	Thr	Asp	Lys	Gln	Ala	Leu	His	Ser	Glu	Ile	Ile	Phe	
		195					200					205				
gtg	caa	tcc	gaa	aaa	gat	ggc	gtc	caa	gtt	gaa	gct	gca	ttg	caa	tgg	672

Val Gln Ser Glu Lys Asp Gly Val Gln Val Glu Ala Ala Leu Gln Trp
 210 215 220

tgc gtt gac gcc tac agc gac aac att ctg ggc ttt gcc aac aac atc 720
 Cys Val Asp Ala Tyr Ser Asp Asn Ile Leu Gly Phe Ala Asn Asn Ile
 225 230 235 240

cgc acg att gac ggc ggc acc cat att gag ggg ctc aaa act gtt ctg 768
 Arg Thr Ile Asp Gly Gly Thr His Ile Glu Gly Leu Lys Thr Val Leu
 245 250 255

acg cgg acg atg aac acg atc gcc cgc aaa cgg aat aaa cgc aag gat 816
 Thr Arg Thr Met Asn Thr Ile Ala Arg Lys Arg Asn Lys Arg Lys Asp
 260 265 270

gcc gac aat aac ctg tcg ggc gag aat att cgc gaa ggg tta aca gcg 864
 Ala Asp Asn Asn Leu Ser Gly Glu Asn Ile Arg Glu Gly Leu Thr Ala
 275 280 285

atc gtt tcg gtc aaa gtt ccg gat ccg gaa ttt gaa ggg caa acc aaa 912
 Ile Val Ser Val Lys Val Pro Asp Pro Glu Phe Glu Gly Gln Thr Lys
 290 295 300

aca aag ctc ggc aat acc gaa gtt cgc ggc atc gtc gat acg ctc gtg 960
 Thr Lys Leu Gly Asn Thr Glu Val Arg Gly Ile Val Asp Thr Leu Val
 305 310 315 320

ggc gaa acg ttg acg gaa tat ctg gaa ttc cat ccc agc gtt gcc gat 1008
 Gly Glu Thr Leu Thr Glu Tyr Leu Glu Phe His Pro Ser Val Ala Asp
 325 330 335

ttg atc ctc gaa aaa gcg att caa gcc ttt aat gcg gct gag gca gcg 1056
 Leu Ile Leu Glu Lys Ala Ile Gln Ala Phe Asn Ala Ala Glu Ala Ala
 340 345 350

cga cgg gca cgg gaa ttg gtg cgt cgc aaa tca gtg ctg gaa tct tcg 1104
 Arg Arg Ala Arg Glu Leu Val Arg Arg Lys Ser Val Leu Glu Ser Ser
 355 360 365

aca ttg ccc ggt aaa tta gca gac tgt tcc agt cgc gat ccc ggt gaa 1152
 Thr Leu Pro Gly Lys Leu Ala Asp Cys Ser Ser Arg Asp Pro Gly Glu
 370 375 380

tct gaa atc ttc atc gtg 1170
 Ser Glu Ile Phe Ile Val
 385 390

<210> 14
 <211> 390
 <212> PRT
 <213> Synechococcus sp.

<400> 14
 Val Val Asp Asn Ala Val Asp Lys Ala Leu Ala Gly Tyr Cys Asn Thr
 1 5 10 15
 Ile Asp Val Arg Leu Leu Lys Asp Gly Ser Cys Gln Val Thr Asp Asn
 20 25 30

Gly	Arg	Gly	Ile	Pro	Thr	Asp	Ile	His	Pro	Gln	Thr	Gly	Lys	Ser	Ala
		35					40					45			
Leu	Glu	Thr	Val	Leu	Thr	Ile	Leu	His	Ala	Gly	Gly	Lys	Phe	Gly	Gly
	50					55					60				
Gly	Gly	Tyr	Lys	Val	Ser	Gly	Gly	Leu	His	Gly	Val	Gly	Val	Ser	Val
65					70					75				80	
Val	Asn	Ala	Leu	Ser	Glu	Tyr	Val	Glu	Val	Thr	Val	Trp	Arg	Glu	Gly
				85					90					95	
Lys	Thr	His	Gln	Arg	Phe	Glu	Gln	Gly	Asn	Pro	Ile	Gly	Glu	Leu	
		100					105					110			
Gln	Val	Ala	Pro	Asp	Ala	Asp	Asp	Arg	Arg	Gly	Thr	Gln	Val	Arg	Phe
	115						120					125			
Lys	Pro	Asp	Ala	Thr	Ile	Phe	Ser	Glu	Thr	Thr	Glu	Phe	Asp	Tyr	Gly
130						135					140				
Thr	Leu	Ala	Ser	Arg	Leu	Lys	Glu	Leu	Ala	Tyr	Leu	Asn	Ala	Gly	Val
145					150					155				160	
Arg	Ile	Asp	Phe	Thr	Asp	Glu	Arg	Leu	Gln	Leu	Thr	Lys	Asn	His	Glu
				165					170					175	
Pro	His	Gln	Glu	Thr	Tyr	Tyr	Phe	Glu	Gly	Gly	Ile	Arg	Glu	Tyr	Val
		180					185						190		
Ala	Tyr	Met	Asn	Thr	Asp	Lys	Gln	Ala	Leu	His	Ser	Glu	Ile	Ile	Phe
	195						200					205			
Val	Gln	Ser	Glu	Lys	Asp	Gly	Val	Gln	Val	Glu	Ala	Ala	Leu	Gln	Trp
210						215					220				
Cys	Val	Asp	Ala	Tyr	Ser	Asp	Asn	Ile	Leu	Gly	Phe	Ala	Asn	Asn	Ile
225					230					235				240	
Arg	Thr	Ile	Asp	Gly	Gly	Thr	His	Ile	Glu	Gly	Leu	Lys	Thr	Val	Leu
				245					250					255	
Thr	Arg	Thr	Met	Asn	Thr	Ile	Ala	Arg	Lys	Arg	Asn	Lys	Arg	Lys	Asp
		260					265						270		
Ala	Asp	Asn	Asn	Leu	Ser	Gly	Glu	Asn	Ile	Arg	Glu	Gly	Leu	Thr	Ala
	275						280					285			
Ile	Val	Ser	Val	Lys	Val	Pro	Asp	Pro	Glu	Phe	Glu	Gly	Gln	Thr	Lys
290						295					300				
Thr	Lys	Leu	Gly	Asn	Thr	Glu	Val	Arg	Gly	Ile	Val	Asp	Thr	Leu	Val
305					310					315				320	
Gly	Glu	Thr	Leu	Thr	Glu	Tyr	Leu	Glu	Phe	His	Pro	Ser	Val	Ala	Asp
				325					330					335	
Leu	Ile	Leu	Glu	Lys	Ala	Ile	Gln	Ala	Phe	Asn	Ala	Ala	Glu	Ala	Ala
				340				345					350		
Arg	Arg	Ala	Arg	Glu	Leu	Val	Arg	Arg	Lys	Ser	Val	Leu	Glu	Ser	Ser
		355					360					365			
Thr	Leu	Pro	Gly	Lys	Leu	Ala	Asp	Cys	Ser	Ser	Arg	Asp	Pro	Gly	Glu
370					375						380				
Ser	Glu	Ile	Phe	Ile	Val										
385					390										

<210> 15

<211> 696

<212> DNA

<213> Caulobacter crescentus

<220>

<221> CDS

<222> (1)...(696)

<400> 15

cag aac agc tac aag gtc tcg ggc ggt ctg cac ggc gtg ggc gtc tcg Gln Asn Ser Tyr Lys Val Ser Gly Gly Leu His Gly Val Gly Val Ser	48
1 5 10 15	
gtc gtg aac gcc ctg tcg gat tgg ctg gag ctg ctg atc cac cgc aac Val Val Asn Ala Leu Ser Asp Trp Leu Glu Leu Leu Ile His Arg Asn	96
20 25 30	
ggc aag gtc cac cag atg cgc ttc gag cgc ggc gac gcg gtc acc tcg Gly Lys Val His Gln Met Arg Phe Glu Arg Gly Asp Ala Val Thr Ser	144
35 40 45	
ctg aag gtc acc ggc gac tcg ccc gtg cgg acc gag ggc ccc aag gcc Leu Lys Val Thr Gly Asp Ser Pro Val Arg Thr Glu Gly Pro Lys Ala	192
50 55 60	
ggc gag acc ctg acc ggt acg gaa gtt acg ttc ttt ccg tcg aag gac Gly Glu Thr Leu Thr Gly Thr Glu Val Thr Phe Phe Pro Ser Lys Asp	240
65 70 75 80	
acc ttc gcc ttc atc gaa ttc gac cgg aag acg ctg gag cac cgc ctg Thr Phe Ala Phe Ile Glu Phe Asp Arg Lys Thr Leu Glu His Arg Leu	288
85 90 95	
cgc gag ctg gcc ttc ctg aac tcg ggc gtg acg atc tgg ttc aag gac Arg Glu Leu Ala Phe Leu Asn Ser Gly Val Thr Ile Trp Phe Lys Asp	336
100 105 110	
cat cgc gac gtc gag ccg tgg gaa gag aag ctg ttc tac gag ggc ggc His Arg Asp Val Glu Pro Trp Glu Glu Lys Leu Phe Tyr Glu Gly Gly	384
115 120 125	
atc gag gcc ttc gtg cgc cac ctc gac aag gcc aag acg ccg ctg ctg Ile Glu Ala Phe Val Arg His Leu Asp Lys Ala Lys Thr Pro Leu Leu	432
130 135 140	
aag gcc ccg atc gcc gtc aag ggc gtc aag gac aag gtc gag atc gac Lys Ala Pro Ile Ala Val Lys Gly Val Lys Asp Lys Val Glu Ile Asp	480
145 150 155 160	
ctg gcc ctg tgg tgg aac gac agc tac cac gag cag atg ctg tgc ttc Leu Ala Leu Trp Trp Asn Asp Ser Tyr His Glu Gln Met Leu Cys Phe	528
165 170 175	
acc aac aac atc ccg cag ccg gat ggc ggc acg cac ctg tcg gcc ttt Thr Asn Asn Ile Pro Gln Arg Asp Gly Gly Thr His Leu Ser Ala Phe	576
180 185 190	
cgc gcg gcc ctg acc ccg atc atc acc agc tac gcc gag agc tcc ggc Arg Ala Ala Leu Thr Arg Ile Ile Thr Ser Tyr Ala Glu Ser Ser Gly	624
195 200 205	
atc ctg aag aag gaa aag gtc agc ctg ggc ggc gaa gac agc cgc gag Ile Leu Lys Lys Glu Lys Val Ser Leu Gly Gly Glu Asp Ser Arg Glu	672
210 215 220	
ggc ctg acc tgc gtg ctg tcg gtc	696

Gly Leu Thr Cys Val Leu Ser Val
225 230

<210> 16
<211> 232
<212> PRT
<213> *Caulobacter crescentus*

<400> 16
Gln Asn Ser Tyr Lys Val Ser Gly Gly Leu His Gly Val Gly Val Ser
1 5 10 15
Val Val Asn Ala Leu Ser Asp Trp Leu Glu Leu Leu Ile His Arg Asn
20 25 30
Gly Lys Val His Gln Met Arg Phe Glu Arg Gly Asp Ala Val Thr Ser
35 40 45
Leu Lys Val Thr Gly Asp Ser Pro Val Arg Thr Glu Gly Pro Lys Ala
50 55 60
Gly Glu Thr Leu Thr Gly Thr Glu Val Thr Phe Phe Pro Ser Lys Asp
65 70 75 80
Thr Phe Ala Phe Ile Glu Phe Asp Arg Lys Thr Leu Glu His Arg Leu
85 90 95
Arg Glu Leu Ala Phe Leu Asn Ser Gly Val Thr Ile Trp Phe Lys Asp
100 105 110
His Arg Asp Val Glu Pro Trp Glu Glu Lys Leu Phe Tyr Glu Gly Gly
115 120 125
Ile Glu Ala Phe Val Arg His Leu Asp Lys Ala Lys Thr Pro Leu Leu
130 135 140
Lys Ala Pro Ile Ala Val Lys Gly Val Lys Asp Lys Val Glu Ile Asp
145 150 155 160
Leu Ala Leu Trp Trp Asn Asp Ser Tyr His Glu Gln Met Leu Cys Phe
165 170 175
Thr Asn Asn Ile Pro Gln Arg Asp Gly Gly Thr His Leu Ser Ala Phe
180 185 190
Arg Ala Ala Leu Thr Arg Ile Ile Thr Ser Tyr Ala Glu Ser Ser Gly
195 200 205
Ile Leu Lys Lys Glu Lys Val Ser Leu Gly Gly Glu Asp Ser Arg Glu
210 215 220
Gly Leu Thr Cys Val Leu Ser Val
225 230

<210> 17
<211> 888
<212> DNA
<213> *Pseudomonas putida*

<220>
<221> CDS
<222> (1)...(888)

<400> 17
ggc ggc ctg cac ggt gta ggc gtg tgc gta gtg aac gca ctg tct gaa 48
Gly Gly Leu His Gly Val Gly Val Ser Val Val Asn Ala Leu Ser Glu
1 5 10 15
gag ctc gtc ctc acc gtt cgc cgt agc ggc aag atc tgg gaa cag acc 96
Glu Leu Val Leu Thr Val Arg Arg Ser Gly Lys Ile Trp Glu Gln Thr
20 25 30

tac gtc cat ggt gtt ccg cag gaa ccg atg aag atc gtt ggc gac agc Tyr Val His Gly Val Pro Gln Glu Pro Met Lys Ile Val Gly Asp Ser 35 40 45	144
gaa acc acc ggc acc cag atc cac ttc aag gct tcc agc gaa acc ttc Glu Thr Thr Gly Thr Gln Ile His Phe Lys Ala Ser Ser Glu Thr Phe 50 55 60	192
aag aac atc cac ttc agc tgg gac atc ctg gcc aag cgg att cgt gaa Lys Asn Ile His Phe Ser Trp Asp Ile Leu Ala Lys Arg Ile Arg Glu 65 70 75 80	240
ctg tcc ttc ctc aac tcc ggt gtc ggc atc gtc ctc aag gat gag cgc Leu Ser Phe Leu Asn Ser Gly Val Gly Ile Val Leu Lys Asp Glu Arg 85 90 95	288
agc ggc aag gaa gaa ctg ttc aag tac gaa ggc ggc ttg cgc gcg ttc Ser Gly Lys Glu Glu Leu Phe Lys Tyr Glu Gly Gly Leu Arg Ala Phe 100 105 110	336
gtt gaa tac ctg aac acc aac aag acc ccg gtc aac cag gtg ttc cat Val Glu Tyr Leu Asn Thr Asn Lys Thr Pro Val Asn Gln Val Phe His 115 120 125	384
ttc aac atc cag cgc gaa gac ggc atc ggc gta gaa atc gcc ctg cag Phe Asn Ile Gln Arg Glu Asp Gly Ile Gly Val Glu Ile Ala Leu Gln 130 135 140	432
tgg aac gac agc ttc aac gag aac ctg ttg tgc ttc acc aac aac att Trp Asn Asp Ser Phe Asn Glu Asn Leu Leu Cys Phe Thr Asn Asn Ile 145 150 155 160	480
ccg cag cgc gat ggc ggt act cac ctg gtg ggt ttc cgt tcc gcc ctg Pro Gln Arg Asp Gly Gly Thr His Leu Val Gly Phe Arg Ser Ala Leu 165 170 175	528
acg cgt aac ctc aat acg tat atc gaa gcc gaa ggc ctg gcg aag aag Thr Arg Asn Leu Asn Thr Tyr Ile Glu Ala Glu Gly Leu Ala Lys Lys 180 185 190	576
cac aag gtc gcg acc acc ggt gac gat gcc cgt gaa ggc ctg gcc gcg His Lys Val Ala Thr Thr Gly Asp Asp Ala Arg Glu Gly Leu Ala Ala 195 200 205	624
atc att tcg gta aaa gtg ccg gat ccg aag ttc agc tcc cag acc aag Ile Ile Ser Val Lys Val Pro Asp Pro Lys Phe Ser Ser Gln Thr Lys 210 215 220	672
gac aag ctg gtt tct tcc gaa gtg aag acc gcg gtc gaa cag gaa atg Asp Lys Leu Val Ser Ser Glu Val Lys Thr Ala Val Glu Gln Glu Met 225 230 235 240	720
ggc aag tac ttc tcc gac ttc ctg ctg gaa aac ccg aac gaa gcc aag Gly Lys Tyr Phe Ser Asp Phe Leu Leu Glu Asn Pro Asn Glu Ala Lys 245 250 255	768

ctg gtt gtc ggc aag atg atc gac gcg gca cgt gct cgt gaa gcg gcg 816
 Leu Val Val Gly Lys Met Ile Asp Ala Ala Arg Ala Arg Glu Ala Ala
 260 265 270

cgc aag acc cgt gag atg acc cgc cgc aaa ggc gcg ctg gac atc gcc 864
 Arg Lys Thr Arg Glu Met Thr Arg Arg Lys Gly Ala Leu Asp Ile Ala
 275 280 285

ggc ctg ccg ggc aaa ctg gct gac 888
 Gly Leu Pro Gly Lys Leu Ala Asp
 290 295

<210> 18
 <211> 296
 <212> PRT
 <213> Pseudomonas putida

<400> 18
 Gly Gly Leu His Gly Val Gly Val Ser Val Val Asn Ala Leu Ser Glu
 1 5 10 15
 Glu Leu Val Leu Thr Val Arg Arg Ser Gly Lys Ile Trp Glu Gln Thr
 20 25 30
 Tyr Val His Gly Val Pro Gln Glu Pro Met Lys Ile Val Gly Asp Ser
 35 40 45
 Glu Thr Thr Gly Thr Gln Ile His Phe Lys Ala Ser Ser Glu Thr Phe
 50 55 60
 Lys Asn Ile His Phe Ser Trp Asp Ile Leu Ala Lys Arg Ile Arg Glu
 65 70 75 80
 Leu Ser Phe Leu Asn Ser Gly Val Gly Ile Val Leu Lys Asp Glu Arg
 85 90 95
 Ser Gly Lys Glu Glu Leu Phe Lys Tyr Glu Gly Gly Leu Arg Ala Phe
 100 105 110
 Val Glu Tyr Leu Asn Thr Asn Lys Thr Pro Val Asn Gln Val Phe His
 115 120 125
 Phe Asn Ile Gln Arg Glu Asp Gly Ile Gly Val Glu Ile Ala Leu Gln
 130 135 140
 Trp Asn Asp Ser Phe Asn Glu Asn Leu Leu Cys Phe Thr Asn Asn Ile
 145 150 155 160
 Pro Gln Arg Asp Gly Gly Thr His Leu Val Gly Phe Arg Ser Ala Leu
 165 170 175
 Thr Arg Asn Leu Asn Thr Tyr Ile Glu Ala Glu Gly Leu Ala Lys Lys
 180 185 190
 His Lys Val Ala Thr Thr Gly Asp Asp Ala Arg Glu Gly Leu Ala Ala
 195 200 205
 Ile Ile Ser Val Lys Val Pro Asp Pro Lys Phe Ser Ser Gln Thr Lys
 210 215 220
 Asp Lys Leu Val Ser Ser Glu Val Lys Thr Ala Val Glu Gln Glu Met
 225 230 235 240
 Gly Lys Tyr Phe Ser Asp Phe Leu Leu Glu Asn Pro Asn Glu Ala Lys
 245 250 255
 Leu Val Val Gly Lys Met Ile Asp Ala Ala Arg Ala Arg Glu Ala Ala
 260 265 270
 Arg Lys Thr Arg Glu Met Thr Arg Arg Lys Gly Ala Leu Asp Ile Ala
 275 280 285
 Gly Leu Pro Gly Lys Leu Ala Asp
 290 295

<210> 19
 <211> 531
 <212> DNA
 <213> Synechococcus sp.

<220>
 <221> CDS
 <222> (1)...(531)

<400> 19
 ttg gtg cgt cgc aaa tca gtg ctg gaa tct tcg aca ttg ccc ggt aaa 48
 Leu Val Arg Arg Lys Ser Val Leu Glu Ser Ser Thr Leu Pro Gly Lys
 1 5 10 15

tta gca gac tgt tcc agt cgc gat ccc ggt gaa tct gaa atc ttc atc 96
 Leu Ala Asp Cys Ser Ser Arg Asp Pro Gly Glu Ser Glu Ile Phe Ile
 20 25 30

gtg gaa ggg gat tcg gca ggt ggc agt gct aaa cag ggg cgc gat cgc 144
 Val Glu Gly Asp Ser Ala Gly Gly Ser Ala Lys Gln Gly Arg Asp Arg
 35 40 45

cgc ttc caa gcc atc ctg cct ctg cgc ggc aaa atc ctc aac atc gag 192
 Arg Phe Gln Ala Ile Leu Pro Leu Arg Gly Lys Ile Leu Asn Ile Glu
 50 55 60

aaa acg gac gat gcc aaa atc tac aaa aac act gag atc caa gcc ctg 240
 Lys Thr Asp Asp Ala Lys Ile Tyr Lys Asn Thr Glu Ile Gln Ala Leu
 65 70 75 80

att aca gcg ctg ggc ctc gga att aaa ggg gag gaa ttt gat gct tcc 288
 Ile Thr Ala Leu Gly Leu Gly Ile Lys Gly Glu Glu Phe Asp Ala Ser
 85 90 95

caa ctg cgc tac cac cgt att gtg atc atg act gac gcg gac gtc gat 336
 Gln Leu Arg Tyr His Arg Ile Val Ile Met Thr Asp Ala Asp Val Asp
 100 105 110

ggt gcg cac atc cgt acc ctc ttg ctc acc ttc ttc tat cgc tat cag 384
 Gly Ala His Ile Arg Thr Leu Leu Leu Thr Phe Phe Tyr Arg Tyr Gln
 115 120 125

cga tcg ctg ctg gag cag ggc tac atg tac att gcc tgc ccg ccg ctg 432
 Arg Ser Leu Leu Glu Gln Gly Tyr Met Tyr Ile Ala Cys Pro Pro Leu
 130 135 140

tac aag ttg gag cgg gga cgt aat cac tac tat tgc tac aac gaa cgc 480
 Tyr Lys Leu Glu Arg Gly Arg Asn His Tyr Tyr Cys Tyr Asn Glu Arg
 145 150 155 160

gaa ctg cag gaa cgg att gcg acg ttc cct gaa aac gcc aac tat acg 528
 Glu Leu Gln Glu Arg Ile Ala Thr Phe Pro Glu Asn Ala Asn Tyr Thr
 165 170 175

att 531
 Ile

<210> 20
 <211> 177
 <212> PRT
 <213> *Synechococcus* sp.

<400> 20
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 1 5 10 15
 Leu Ala Asp Cys Ser Ser Arg Asp Pro Gly Glu Ser Glu Ile Phe Ile
 20 25 30
 Val Glu Gly Asp Ser Ala Gly Gly Ser Ala Lys Gln Gly Arg Asp Arg
 35 40 45
 Arg Phe Gln Ala Ile Leu Pro Leu Arg Gly Lys Ile Leu Asn Ile Glu
 50 55 60
 Lys Thr Asp Asp Ala Lys Ile Tyr Lys Asn Thr Glu Ile Gln Ala Leu
 65 70 75 80
 Ile Thr Ala Leu Gly Leu Gly Ile Lys Gly Glu Glu Phe Asp Ala Ser
 85 90 95
 Gln Leu Arg Tyr His Arg Ile Val Ile Met Thr Asp Ala Asp Val Asp
 100 105 110
 Gly Ala His Ile Arg Thr Leu Leu Leu Thr Phe Phe Tyr Arg Tyr Gln
 115 120 125
 Arg Ser Leu Leu Glu Gln Gly Tyr Met Tyr Ile Ala Cys Pro Pro Leu
 130 135 140
 Tyr Lys Leu Glu Arg Gly Arg Asn His Tyr Tyr Cys Tyr Asn Glu Arg
 145 150 155 160
 Glu Leu Gln Glu Arg Ile Ala Thr Phe Pro Glu Asn Ala Asn Tyr Thr
 165 170 175
 Ile

<210> 21
 <211> 660
 <212> DNA
 <213> *Caulobacter crescentus*

<220>
 <221> CDS
 <222> (1)...(660)

<400> 21
 cgg gat ggc ggc acg cac ctg tcg gcc ttt cgc gcg gcc ctg acc cgg 48
 Arg Asp Gly Gly Thr His Leu Ser Ala Phe Arg Ala Ala Leu Thr Arg
 1 5 10 15
 atc atc acc agc tac gcc gag agc tcc ggc atc ctg aag aag gaa aag 96
 Ile Ile Thr Ser Tyr Ala Glu Ser Ser Gly Ile Leu Lys Lys Glu Lys
 20 25 30
 gtc agc ctg ggc ggc gaa gac agc cgc gag ggc ctg acc tgc gtg ctg 144
 Val Ser Leu Gly Gly Glu Asp Ser Arg Glu Gly Leu Thr Cys Val Leu
 35 40 45
 tcg gtc aag gtc ccg gat ccg aag ttc agc tgc cag acc aag gac aag 192
 Ser Val Lys Val Pro Asp Pro Lys Phe Ser Ser Gln Thr Lys Asp Lys
 50 55 60

ctg gtc tcg tcc gaa gtg cgc ccc gcc gtt gag ggc ctg gtg tcg gaa 240
 Leu Val Ser Ser Glu Val Arg Pro Ala Val Glu Gly Leu Val Ser Glu
 65 70 75 80

ggt ctc tcg acc tgg ttc gag gaa cat ccg aac gag gcc aag gcg atc 288
 Gly Leu Ser Thr Trp Phe Glu Glu His Pro Asn Glu Ala Lys Ala Ile
 85 90 95

gtg acc aag atc gcc gag gcc gcc gcc gcc cgc gag gcc gcc cgc aag 336
 Val Thr Lys Ile Ala Glu Ala Ala Ala Ala Arg Glu Ala Ala Arg Lys
 100 105 110

gcg cga gag ctg acc cgc cgc aag agc gcg ctc gac atc acc agc ctg 384
 Ala Arg Glu Leu Thr Arg Arg Lys Ser Ala Leu Asp Ile Thr Ser Leu
 115 120 125

ccc ggc aag ctc gcc gac tgc tcg gaa cgc gat ccg gcc aag tcc gag 432
 Pro Gly Lys Leu Ala Asp Cys Ser Glu Arg Asp Pro Ala Lys Ser Glu
 130 135 140

atc ttc atc gtc gag ggc gac tcg gcg ggc ggc tcg gcc aag cag gcc 480
 Ile Phe Ile Val Glu Gly Asp Ser Ala Gly Gly Ser Ala Lys Gln Ala
 145 150 155 160

cgc aac cgc gac aac cag gcc gtt ctg ccc ctg cgc ggc aag atc ctg 528
 Arg Asn Arg Asp Asn Gln Ala Val Leu Pro Leu Arg Gly Lys Ile Leu
 165 170 175

aac gtc gag cgg gcc cgc ttc gac aag atg ctg tcg tcc gac cag atc 576
 Asn Val Glu Arg Ala Arg Phe Asp Lys Met Leu Ser Ser Asp Gln Ile
 180 185 190

ggc acg ctg atc acc gcc ctg ggc gcg ggg atc ggc cgc gac gac ttc 624
 Gly Thr Leu Ile Thr Ala Leu Gly Ala Gly Ile Gly Arg Asp Asp Phe
 195 200 205

aac ccg gac aag gtg cgc tac cac aag atc gtg ctg 660
 Asn Pro Asp Lys Val Arg Tyr His Lys Ile Val Leu
 210 215 220

<210> 22

<211> 220

<212> PRT

<213> *Caulobacter crescentus*

<400> 22

Arg Asp Gly Gly Thr His Leu Ser Ala Phe Arg Ala Ala Leu Thr Arg
 1 5 10 15

Ile Ile Thr Ser Tyr Ala Glu Ser Ser Gly Ile Leu Lys Lys Glu Lys
 20 25 30

Val Ser Leu Gly Gly Glu Asp Ser Arg Glu Gly Leu Thr Cys Val Leu
 35 40 45

Ser Val Lys Val Pro Asp Pro Lys Phe Ser Ser Gln Thr Lys Asp Lys
 50 55 60

Leu Val Ser Ser Glu Val Arg Pro Ala Val Glu Gly Leu Val Ser Glu
 65 70 75 80

ttt tta tct gaa gtt ttt tac tct gaa gaa gga cta aaa gaa ttt att	384
Phe Leu Ser Glu Val Phe Tyr Ser Glu Glu Gly Leu Lys Glu Phe Ile	
115 120 125	
aag ttt tta gac ggt aac aga gaa caa cta ata cgt gat gtt gtt tca	432
Lys Phe Leu Asp Gly Asn Arg Glu Gln Leu Ile Arg Asp Val Val Ser	
130 135 140	
atg gaa ggt gaa aaa aac gga att cct gtt gag gtt gca atg gtg tac	480
Met Glu Gly Glu Lys Asn Gly Ile Pro Val Glu Val Ala Met Val Tyr	
145 150 155 160	
aat aca tca tat tca gaa aat ctt cac tct tac gta aat aat att aat	528
Asn Thr Ser Tyr Ser Glu Asn Leu His Ser Tyr Val Asn Asn Ile Asn	
165 170 175	
aca cat gaa ggt ggt aca cac ctt tca ggt ttt aga aga ggt tta aca	576
Thr His Glu Gly Gly Thr His Leu Ser Gly Phe Arg Arg Gly Leu Thr	
180 185 190	
tca acc tta aaa aag tat gca gat gca tct gga atg tta gac aaa tta	624
Ser Thr Leu Lys Lys Tyr Ala Asp Ala Ser Gly Met Leu Asp Lys Leu	
195 200 205	
aag ttt gag att cag gga gat gat ttt aga gaa ggt tta acg gct att	672
Lys Phe Glu Ile Gln Gly Asp Phe Arg Glu Gly Leu Thr Ala Ile	
210 215 220	
gtg tct gtt aaa gtt gca gaa cct cag ttt gaa ggg caa aca aaa act	720
Val Ser Val Lys Val Ala Glu Pro Gln Phe Glu Gly Gln Thr Lys Thr	
225 230 235 240	
aaa tta ggt aac aga gaa gtt tct tct gca gtg agc caa gct gta tca	768
Lys Leu Gly Asn Arg Glu Val Ser Ser Ala Val Ser Gln Ala Val Ser	
245 250 255	
gaa atg ctt acc aac tat tta gaa gaa aac cca gat gat gct aag gta	816
Glu Met Leu Thr Asn Tyr Leu Glu Glu Asn Pro Asp Asp Ala Lys Val	
260 265 270	
att gta caa aaa gtc att ttg gca gcg caa gca cgt cat gcg gct aca	864
Ile Val Gln Lys Val Ile Leu Ala Ala Gln Ala Arg His Ala Ala Thr	
275 280 285	
aaa gcc cgt gaa atg gta cag cgt aaa acg gta atg agt ata ggt ggt	912
Lys Ala Arg Glu Met Val Gln Arg Lys Thr Val Met Ser Ile Gly Gly	
290 295 300	
tta cca ggg aaa tta tca gac tgt tct gag caa gat gct aca aaa tgc	960
Leu Pro Gly Lys Leu Ser Asp Cys Ser Glu Gln Asp Ala Thr Lys Cys	
305 310 315 320	
gaa gta ttc ctt gta gag gga gat tcg gcg ggt ggt act gct aaa caa	1008
Glu Val Phe Leu Val Glu Gly Asp Ser Ala Gly Gly Thr Ala Lys Gln	
325 330 335	
ggt agg gac aga aac ttt cag gca ata tta ccg ctt cgt ggt aaa atc	1056

Gly Arg Asp Arg Asn Phe Gln Ala Ile Leu Pro Leu Arg Gly Lys Ile
 340 345 350
 tta aat gtt gaa aaa gca atg caa cat aag gtt ttt gaa aac gaa gaa 1104
 Leu Asn Val Glu Lys Ala Met Gln His Lys Val Phe Glu Asn Glu Glu
 355 360 365
 ata aaa aat att tac aca gct tta ggt gtt act att ggt aca gaa gaa 1152
 Ile Lys Asn Ile Tyr Thr Ala Leu Gly Val Thr Ile Gly Thr Glu Glu
 370 375 380
 gat agt aaa gcc tta aac tta gaa aaa tta aga tac cat aaa gta gtt 1200
 Asp Ser Lys Ala Leu Asn Leu Glu Lys Leu Arg Tyr His Lys Val Val
 385 390 395 400
 att atg tgt gat gcc gat gta gat ggt agc cac att gaa act tta atc 1248
 Ile Met Cys Asp Ala Asp Val Asp Gly Ser His Ile Glu Thr Leu Ile
 405 410 415
 ctt aca ttc ttc ttc cgt ttt atg agg gag tta ata gaa ggc ggt cac 1296
 Leu Thr Phe Phe Phe Arg Phe Met Arg Glu Leu Ile Glu Gly Gly His
 420 425 430
 gtt tat ata gca acc cca cct tta tac ttg gta aaa aag gga aca aaa 1344
 Val Tyr Ile Ala Thr Pro Pro Leu Tyr Leu Val Lys Lys Gly Thr Lys
 435 440 445
 aaa cgt tat gct tgg aat gat aaa gaa cga gat gag ata gca gaa agc 1392
 Lys Arg Tyr Ala Trp Asn Asp Lys Glu Arg Asp Glu Ile Ala Glu Ser
 450 455 460
 ttt aat ggt agt gtt ggt ata caa aga tat 1422
 Phe Asn Gly Ser Val Gly Ile Gln Arg Tyr
 465 470

<210> 24

<211> 474

<212> PRT

<213> *Cytophaga lytica*

<400> 24

Asp Lys Asp Ser Tyr Lys Val Ser Gly Gly Leu His Gly Val Gly Val
 1 5 10 15
 Ser Cys Val Asn Ala Leu Ser Asn Asn Leu Lys Ala Thr Val Tyr Arg
 20 25 30
 Glu Gly Lys Ile Trp Glu Gln Glu Tyr Glu Arg Gly Lys Ala Leu Tyr
 35 40 45
 Pro Val Lys Ser Ile Gly Glu Thr Glu Glu Thr Gly Thr Ile Val Thr
 50 55 60
 Phe Tyr Pro Asp Asp Thr Ile Phe Thr Gln Thr Thr Glu Tyr Asn Tyr
 65 70 75 80
 Glu Thr Leu Ser Asn Arg Met Arg Glu Leu Ala Tyr Leu Asn Lys Gly
 85 90 95
 Val Thr Ile Ser Ile Thr Asp Lys Arg Val Lys Asp Glu Lys Gly Glu
 100 105 110
 Phe Leu Ser Glu Val Phe Tyr Ser Glu Glu Gly Leu Lys Glu Phe Ile
 115 120 125

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Lys Phe Leu Asp Gly Asn Arg Glu Gln Leu Ile Arg Asp Val Val Ser
130                      135                      140
Met Glu Gly Glu Lys Asn Gly Ile Pro Val Glu Val Ala Met Val Tyr
145                      150                      155                      160
Asn Thr Ser Tyr Ser Glu Asn Leu His Ser Tyr Val Asn Asn Ile Asn
165                      170                      175
Thr His Glu Gly Gly Thr His Leu Ser Gly Phe Arg Arg Gly Leu Thr
180                      185                      190
Ser Thr Leu Lys Lys Tyr Ala Asp Ala Ser Gly Met Leu Asp Lys Leu
195                      200                      205
Lys Phe Glu Ile Gln Gly Asp Asp Phe Arg Glu Gly Leu Thr Ala Ile
210                      215                      220
Val Ser Val Lys Val Ala Glu Pro Gln Phe Glu Gly Gln Thr Lys Thr
225                      230                      235                      240
Lys Leu Gly Asn Arg Glu Val Ser Ser Ala Val Ser Gln Ala Val Ser
245                      250                      255
Glu Met Leu Thr Asn Tyr Leu Glu Glu Asn Pro Asp Asp Ala Lys Val
260                      265                      270
Ile Val Gln Lys Val Ile Leu Ala Ala Gln Ala Arg His Ala Ala Thr
275                      280                      285
Lys Ala Arg Glu Met Val Gln Arg Lys Thr Val Met Ser Ile Gly Gly
290                      295                      300
Leu Pro Gly Lys Leu Ser Asp Cys Ser Glu Gln Asp Ala Thr Lys Cys
305                      310                      315                      320
Glu Val Phe Leu Val Glu Gly Asp Ser Ala Gly Gly Thr Ala Lys Gln
325                      330                      335
Gly Arg Asp Arg Asn Phe Gln Ala Ile Leu Pro Leu Arg Gly Lys Ile
340                      345                      350
Leu Asn Val Glu Lys Ala Met Gln His Lys Val Phe Glu Asn Glu Glu
355                      360                      365
Ile Lys Asn Ile Tyr Thr Ala Leu Gly Val Thr Ile Gly Thr Glu Glu
370                      375                      380
Asp Ser Lys Ala Leu Asn Leu Glu Lys Leu Arg Tyr His Lys Val Val
385                      390                      395                      400
Ile Met Cys Asp Ala Asp Val Asp Gly Ser His Ile Glu Thr Leu Ile
405                      410                      415
Leu Thr Phe Phe Phe Arg Phe Met Arg Glu Leu Ile Glu Gly Gly His
420                      425                      430
Val Tyr Ile Ala Thr Pro Pro Leu Tyr Leu Val Lys Lys Gly Thr Lys
435                      440                      445
Lys Arg Tyr Ala Trp Asn Asp Lys Glu Arg Asp Glu Ile Ala Glu Ser
450                      455                      460
Phe Asn Gly Ser Val Gly Ile Gln Arg Tyr
465                      470

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<210> 25

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide for PCR

<221> misc_feature

<222> 24, 27, 30

<223> n = A,T,C or G

<400> 25
tgtaaaacga cggccagtca ygcnggnggn aarttyga

38

<210> 26
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated peptide

<400> 26
His Ala Gly Gly Lys Phe Asp
1 5

<210> 27
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide for PCR

<221> misc_feature
<222> 19, 25, 31
<223> n = A,T,C or G

<400> 27
ctgcgttcgt atatgagcnc crtcnacrtc ngcrtc

36

<210> 28
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically generated peptide

<400> 28
Asp Ala Asp Val Asp Gly Ala His Ile Arg Thr Leu
1 5 10

<210> 29
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide for PCR

<221> misc_feature
<222> 27, 30, 33
<223> n = A,T,C or G

<400> 29
gaagtcacga tgaccgttct gcaygsnggn ggnaarttyg g

41

<210> 30
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetically generated peptide

<400> 30
 Glu Val Leu Met Thr Val Leu His Ala Gly Gly Lys Phe Gly
 1 5 10

<210> 31
 <211> 44
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide for PCR

<221> misc_feature
 <222> 27, 33, 39
 <223> n = A,T,C or G

<400> 31
 agcagggtac ggatgtgcga gccrtcnacr tcngrtcng tgat

44

<210> 32
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetically generated peptide

<400> 32
 Met Thr Asp Ala Asp Val Asp Gly Ser His Ile Arg Thr Leu Leu
 1 5 10 15

<210> 33
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide for PCR

<221> misc_feature
 <222> 24, 27, 30
 <223> n = A,T,C or G

<400> 33
 caggaaacag ctatgaccar rtgngtnccn cc

32

<210> 34

<211> 5
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetically generated peptide

<400> 34
 Gly Gly Thr His Leu
 1 5

<210> 35
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide for PCR

<221> misc_feature
 <222> 20, 26, 29, 32
 <223> n = A,T,C or G

<400> 35
 gcaacgagat caacactcmn garggnggna cnca

34

<210> 36
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetically generated peptide

<400> 36
 Asn Asn Ile Asn Thr His Glu Gly Gly Thr His
 1 5 10

<210> 37
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetically generated peptide

<400> 37
 Asn Asn Ile Asn Thr Pro Glu Gly Gly Thr His
 1 5 10

<210> 38
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide for PCR

<221> misc_feature
 <222> 24, 30
 <223> n = A,T,C or G

<400> 38
 tgtaaaacga cggccagtar yttnkyyttt gtytg

35

<210> 39
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetically generated peptide

<400> 39
 Gln Thr Lys Thr Lys Leu
 1 5

<210> 40
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetically generated peptide

<400> 40
 Gln Thr Lys Asp Lys Leu
 1 5

<210> 41
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide for PCR

<221> misc_feature
 <222> 24, 30
 <223> n = A,T,C or G

<400> 41
 taggctagct gaccgtaaga ygcngayrtn gaygg

35

<210> 42
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
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<400> 42
 Asp Ala Asp Val Asp Gly

1 5

<210> 43
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide for PCR

<221> misc_feature
 <222> 25, 28, 31
 <223> n = A,T,C or G

<400> 43
 ccatagctgc gtagcattca tytcnccnar nccytt 36

<210> 44
 <211> 12
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetically generated peptide

<400> 44
 Lys Gly Leu Gly Glu Met Asn Ala Thr Gln Leu Trp
 1 5 10

<210> 45
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
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<221> misc_feature
 <222> 24, 27, 30
 <223> n = A,T,C or G

<400> 45
 caggaaacag ctatgaccaa rmgnccngsn atgtayathg g 41

<210> 46
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetically generated peptide

<400> 46
 Lys Arg Pro Ala Met Tyr Ile Gly
 1 5

<210> 47

<211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetically generated peptide

<400> 47
 Lys Arg Pro Gly Met Tyr Ile Gly
 1 5

<210> 48
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide for PCR

<221> misc_feature
 <222> 21, 24, 27, 33
 <223> n = A,T,C or G

<400> 48
 tgtaaaacga cggccagtcc nccngcnswr tcnccytc

38

<210> 49
 <211> 7
 <212> PRT
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<220>
 <223> synthetically generated peptide

<400> 49
 Glu Gly Asp Ser Ala Gly Gly
 1 5

<210> 50
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide for PCR

<221> misc_feature
 <222> 22, 25, 28, 34
 <223> n = A,T,C or G

<400> 50
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39

<210> 51
 <211> 7
 <212> PRT
 <213> Artificial Sequence

<220>

<223> synthetically generated peptide

<400> 51

Gln Leu Trp Glu Thr Thr Met
1 5

<210> 52

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated peptide

<400> 52

Gln Leu Trp Asp Thr Thr Met
1 5

<210> 53

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide for PCR

<221> misc_feature

<222> 27, 30, 33

<223> n = A,T,C or G

<400> 53

gaagtcacatca tgaccgttct gcaygcnggn ggnaarttyg a

41

<210> 54

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated peptide

<400> 54

Glu Val Ile Met Thr Val Leu His Ala Gly Gly Lys Phe Asp
1 5 10

<210> 55

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated peptide

<400> 55

Glu Val Ile Met Thr Val Leu His Ala Gly Gly Lys Phe Asn

1 5 10
 <210> 56
 <211> 14
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> synthetically generated peptide

 <400> 56
 Glu Val Ile Met Thr Val Leu His Ala Gly Gly Lys Phe Glu
 1 5 10

 <210> 57
 <211> 14
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> synthetically generated peptide

 <400> 57
 Glu Val Ile Met Thr Val Leu His Ala Gly Gly Lys Phe Lys
 1 5 10

 <210> 58
 <211> 38
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> oligonucleotide for PCR

 <221> misc_feature
 <222> 21
 <223> n = A,T,C or G

 <400> 58
 tgtaaaacga cggccagtgc nggrtcytty tcytgrca

 <210> 59
 <211> 7
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> synthetically generated peptide

 <400> 59
 Cys Gln Glu Lys Asp Pro Ala
 1 5

 <210> 60
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>

<223> oligonucleotide for PCR

<221> misc_feature

<222> 26, 38

<223> n = A,T,C or G

<400> 60

gaagtcatca tgaccgttct gcaacnaaya ayathccnca

40

<210> 61

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated peptide

<400> 61

Thr Asn Asn Ile Pro Gln

1

5

<210> 62

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide for PCR

<221> misc_feature

<222> 24, 27, 30, 33

<223> n = A,T,C or G

<400> 62

tgtaaaacga cggccagtaa yttnggntcn ggnacytt

38

<210> 63

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated peptide

<400> 63

Lys Val Pro Asp Pro Lys Phe

1

5

<210> 64

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated peptide

<400> 64
 Lys Val Pro Glu Pro Lys Phe
 1 5

<210> 65
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> oligonucleotide for PCR

<221> misc_feature
 <222> 21, 24, 27, 30, 33
 <223> n = A,T,C or G

<400> 65
 caggaaacag ctatgaccgc nmrmnrngcn mgnga

35

<210> 66
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetically generated peptide

<400> 66
 Ala Arg Arg Ala Arg Glu
 1 5

<210> 67
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetically generated peptide

<400> 67
 Ala Arg Lys Ala Arg Glu
 1 5

<210> 68
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetically generated peptide

<400> 68
 Ala Lys Lys Ala Arg Glu
 1 5

<210> 69

<211> 19
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetically generated peptide

<221> VARIANT
 <222> 1
 <223> Xaa = Pro or Ser

<221> VARIANT
 <222> 2
 <223> Xaa = Ala or Thr

<221> VARIANT
 <222> 3
 <223> Xaa = Ala, Val or Leu

<221> VARIANT
 <222> 4
 <223> Xaa = Glu or Asp

<221> VARIANT
 <222> 5
 <223> Xaa = Val or Thr

<221> VARIANT
 <222> 6
 <223> Xaa = Ile or Val

<221> VARIANT
 <222> 7
 <223> Xaa = Met, Leu or Phe

<221> VARIANT
 <222> 9
 <223> Xaa = Val, Gln or Ile

<221> VARIANT
 <222> 17
 <223> Xaa = Asp or Gly

<221> VARIANT
 <222> 18
 <223> Xaa = Asp, Gly, Asn or Ser

<221> VARIANT
 <222> 19
 <223> Xaa = Ser, Lys, Gly, Asp or Asn

<400> 69
 Xaa Xaa Xaa Xaa Xaa Xaa Thr Xaa Leu His Ala Gly Gly Lys Phe
 1 5 10 15
 Xaa Xaa Xaa

<210> 70
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetically generated peptide

<400> 70
 Gly Gly Thr His
 1

<210> 71
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> synthetically generated peptide

<221> VARIANT
 <222> 1
 <223> Xaa = Ile or Leu

<221> VARIANT
 <222> 10
 <223> Xaa = Ala or Ser

<400> 71
 Xaa Met Thr Asp Ala Asp Val Asp Gly Xaa His Ile Arg Thr Leu
 1 5 10 15

<210> 72
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
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<221> VARIANT
 <222> 5
 <223> Xaa = Gly or Ala

<221> VARIANT
 <222> 10
 <223> Xaa = Ser or Asp

<400> 72
 Arg Lys Arg Pro Xaa Met Tyr Ile Gly Xaa Thr
 1 5 10

<210> 73
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>

<223> synthetically generated peptide

<221> VARIANT

<222> 2

<223> Xaa = Thr or Pro

<221> VARIANT

<222> 3

<223> Xaa = Lys or Asn

<221> VARIANT

<222> 4

<223> Xaa = Thr, Asp, Gly, Lys, Ser, Phe or Tyr

<400> 73

Gln Xaa Xaa Xaa Lys Leu

1 5

<210> 74

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated peptide

<221> VARIANT

<222> 1

<223> Xaa = Tyr or Phe

<221> VARIANT

<222> 9

<223> Xaa = Ala or Pro

<400> 74

Xaa Lys Gly Leu Gly Glu Met Asn Xaa

1 5

<210> 75

<211> 9

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated peptide

<400> 75

Val Glu Gly Asp Ser Ala Gly Gly Ser

1 5

<210> 76

<211> 7

<212> PRT

<213> Artificial Sequence

<220>

<223> synthetically generated peptide

<221> VARIANT

<222> 2

<223> Xaa = His or Val

<221> VARIANT

<222> 6

<223> Xaa = Gln or Lys

<400> 76

Lys Xaa Pro Asp Pro Xaa Phe

1 5

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<221> VARIANT

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<222> 11

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<222> 14

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<400> 77

Leu Pro Gly Lys Leu Ala Asp Cys Xaa Xaa Xaa Asp Pro Xaa

1 5 10

<210> 78

<211> 9

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<221> VARIANT

<222> 3

<223> Xaa = Trp or Arg

<221> VARIANT

<222> 4

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<210> 81
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<210> 82

<211> 8

<212> PRT

<213> *Pseudomonas putida*

<400> 82

Met Thr Asp Ala Asp Val Asp Gly

1

5